

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/937,779B
Source: 1fw/b
Date Processed by STIC: 6/13/06

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/937,779B

DATE: 06/13/2006
TIME: 09:45:31

Input Set : A:\00930003.APP
Output Set: N:\CRF4\06132006\I937779B.raw

3 <110> APPLICANT: DAHLQVIST, ANDERS
4 STAHL, ULF
5 LENMAN, MARIT
6 BANAS, ANTONI
7 RONNE, HANS
8 STYMFNE, STEN
10 <120> TITLE OF INVENTION: PROCESSES FOR PRODUCING TRIACYLGLYCEROL USING GENES
11 THAT ENCODE PHOSPHOLIPID:DIACYLGLYCEROL
12 ACYLTRANSFERASES
14 <130> FILE REFERENCE: 0093/000003
16 <140> CURRENT APPLICATION NUMBER: 09/937,779B
17 <141> CURRENT FILING DATE: 2002-07-02
19 <150> PRIOR APPLICATION NUMBER: PCT/EP00/002701
20 <151> PRIOR FILING DATE: 2000-03-28
22 <150> PRIOR APPLICATION NUMBER: 60/180,687
23 <151> PRIOR FILING DATE: 2000-02-07
25 <150> PRIOR APPLICATION NUMBER: EP 99111321.8
26 <151> PRIOR FILING DATE: 1999-06-10
28 <150> PRIOR APPLICATION NUMBER: EP 99106656.4
29 <151> PRIOR FILING DATE: 1999-04-01
31 <160> NUMBER OF SEQ ID NOS: 35
33 <170> SOFTWARE: PatentIn Ver. 3.3
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 1986
37 <212> TYPE: DNA
38 <213> ORGANISM: Saccharomyces cerevisiae
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)..(1983)
44 <400> SEQUENCE: 1
45 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
46 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
47 1 5 10 15
49 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
50 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
51 20 25 30
53 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
54 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
55 35 40 45
57 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
58 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
59 50 55 60
61 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240

P, 6

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62 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu			
63 65 70 75 80			
65 att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt	288		
66 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe			
67 85 90 95			
69 ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt	336		
70 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe			
71 100 105 110			
73 gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt	384		
74 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val			
75 115 120 125			
77 ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac	432		
78 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn			
79 130 135 140			
81 tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480		
82 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly			
83 145 150 155 160			
85 aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528		
86 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val			
87 165 170 175			
89 atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att	576		
90 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile			
91 180 185 190			
93 gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg	624		
94 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp			
95 195 200 205			
97 gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg	672		
98 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp			
99 210 215 220			
101 ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac	720		
102 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn			
103 225 230 235 240			
105 ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc	768		
106 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile			
107 245 250 255			
109 gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att	816		
110 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile			
111 260 265 270			
113 ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt	864		
114 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu			
115 275 280 285			
117 gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag	912		
118 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys			
119 290 295 300			
121 gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta	960		
122 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu			
123 305 310 315 320			
125 att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg	1008		
126 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp			

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127	325	330	335	
129	gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt			1056
130	Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val			
131	340	345	350	
133	aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc			1104
134	Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly			
135	355	360	365	
137	gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc			1152
138	Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr			
139	370	375	380	
141	att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca			1200
142	Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser			
143	385	390	395	400
145	aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca			1248
146	Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser			
147	405	410	415	
149	atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct			1296
150	Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser			
151	420	425	430	
153	tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att			1344
154	Ser Glu Asp Ala Leu Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile			
155	435	440	445	
157	cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg			1392
158	Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met			
159	450	455	460	
161	aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa			1440
162	Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln			
163	465	470	475	480
165	aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa			1488
166	Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu			
167	485	490	495	
169	gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg			1536
170	Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met			
171	500	505	510	
173	gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac			1584
174	Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr			
175	515	520	525	
177	ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat			1632
178	Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp			
179	530	535	540	
181	gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct			1680
182	Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro			
183	545	550	555	560
185	gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca			1728
186	Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser			
187	565	570	575	
189	atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga			1776
190	Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly			
191	580	585	590	

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193 att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
194 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
195 595 600 605
197 ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
198 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
199 610 615 620
201 gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
202 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
203 625 630 635 640
205 ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
206 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
207 645 650 655
209 atg ccc ttc cca atg taa 1986
210 Met Pro Phe Pro Met
211 660
214 <210> SEQ ID NO: 2
215 <211> LENGTH: 661
216 <212> TYPE: PRT
217 <213> ORGANISM: *Saccharomyces cerevisiae*
219 <400> SEQUENCE: 2
220 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
221 1 5 10 15
223 Asp Glu Asn Asn Lys Gly Ser Val His Asn Lys Arg Glu Ser Arg
224 20 25 30
226 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
227 35 40 45
229 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
230 50 55 60
232 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
233 65 70 75 80
235 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
236 85 90 95
238 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
239 100 105 110
241 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
242 115 120 125
244 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
245 130 135 140
247 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
248 145 150 155 160
250 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
251 165 170 175
253 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
254 180 185 190
256 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
257 195 200 205
259 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
260 210 215 220
262 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn

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263	225	230	235	240												
265	Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile
266																255
268																
269																270
271	Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu
272																285
274																
275																300
277	Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu
278																320
280																
281																335
283	Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val
284																350
286	Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly
287																365
289	Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr
290																380
292	Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser
293																400
295	Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser
296																415
298	Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser
299																430
301	Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile
302																445
304	Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met
305																460
307	Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln
308																480
310	Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu
311																495
313	Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met
314																510
316	Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr
317																525
319	Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp
320																540
322	Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro
323																560
325	Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser
326																575
328	Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly
329																590
331	Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp
332																605
334	Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser
335																620

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2363
Seq#:7; N Pos. 601,627
Seq#:9; N Pos. 15,45,83,103,107,112,210
Seq#:25; N Pos. 240,385
Seq#:25; Xaa Pos. 41,89
Seq#:26; N Pos. 601,627
Seq#:28; N Pos. 15,45,83,103,107,112,210
Seq#:32; Xaa Pos. 2
Seq#:35; Xaa Pos. 41,89

VERIFICATION SUMMARY

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L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2340
L:710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:565
M:341 Repeated in SeqNo=7
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:2328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:215
M:341 Repeated in SeqNo=25
L:2404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:565
M:341 Repeated in SeqNo=26
L:2482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:2636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:2689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:32
M:341 Repeated in SeqNo=35